

Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=1; day=27; hr=10; min=15; sec=52; ms=475;]

=====
=====

Reviewer Comments:

1.

E321 No. of Bases conflict, this line has no nucleotides
SEQID (2) POS (464)

E355 Empty lines found between the amino acid numbering and
the proteins SEQID (2)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (2) POS (464)

W112 Upper case found in data; Found at position(0) SeqId(2)

W112 Upper case found in data; Found at position(1) SeqId(2)

W112 Upper case found in data; Found at position(2) SeqId(2)

W112 Upper case found in data: Found at position(3) SegId(2)

E259 Found undefined lettercode; POS (5) SEQID (2)

E259 Found undefined lettercode: POS (6) SEQID (2)

E259 Found undefined lettercode: POS (7) SEOID (2)

E259 Found undefined lettercode: POS (8) SEQID (2)

E259 Found undefined lettercode: POS (9) SEQID (2)

E259 Found undefined lettercode: POS (10) SEQID (2)

E259 Found undefined lettercode: POS (11) SEQID(2)

E259 Found undefined lettercode: POS (12) SEQID(?)

E259 Found undefined lettercode; POS (13) SEQID(?)

<210> 2

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Peptide sequence of double mutant His310-H435Lys.

<400> 2

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

4

1

WASH_6680526.1

The Sequence Listing file must end at the bottom of the last SEQ ID #. There can be no extra information following the last SEQ ID # in the file. Please remove extra information, "4", "1", and "WASH_6680526.1" found at the end of the file, after SEQ ID # 2.

2.

<110> LABORATOIRE FRANÇAIS DU FRACTIONNEMENT ET DES

BIOTECHNOLOGIES

BOUREL, Dominique

GLACET, Arnaud

JORIEUX, Sylvie

STURA, Enrico

DUCANCEL, Frédéric

TEILLAUD, Jean-Luc

<120> USE OF METALLIC CATIONS TO IMPROVE FUNCTIONAL ACTIVITY

OF ANTIBODIES

<130> D 21 711 NT

<140> 10576440

<141> 2010-01-08

<150> PCT/FR2004/002687

<151> 2004-10-20

<150> FR 03 12228

<151> 2003-10-20

<160> 2

<170> PatentIn version 3.3

The sequence listing must be in ASCII text format. This file contains non-ASCII text characters, see numeric identifier <110> the accent marks in the name "Frédéric". Please make all changes necessary to convert this file to ASCII text only.

Application No: 10576440 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-01-08 14:18:39.238
Finished: 2010-01-08 14:18:43.864
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 626 ms
Total Warnings: 4
Total Errors: 13
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)
W 112	Upper case found in data; Found at position(0) SeqId(2)
W 112	Upper case found in data; Found at position(1) SeqId(2)
W 112	Upper case found in data; Found at position(2) SeqId(2)
W 112	Upper case found in data; Found at position(3) SeqId(2)
E 259	Found undefined lettercode; POS (5) SEQID(2)
E 259	Found undefined lettercode; POS (6) SEQID(2)
E 259	Found undefined lettercode; POS (7) SEQID(2)
E 259	Found undefined lettercode; POS (8) SEQID(2)
E 259	Found undefined lettercode; POS (9) SEQID(2)
E 259	Found undefined lettercode; POS (10) SEQID(2)
E 259	Found undefined lettercode; POS (11) SEQID(2)
E 259	Found undefined lettercode; POS (12) SEQID(2)
E 259	Found undefined lettercode; POS (13) SEQID(2)

<210> 1
<211> 1428
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA sequence of double mutant His310-435Lys

<400> 1
atggagttg ggctgagctg gttttccctc gttgtcttt taagagggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcggt gtccagcctg ggaggtccct gagactctcc 120

tgtacagcct ctggattcac cttcaaaaac tatgttatgc attgggtccg ccaggctcca 180

gccaaggggc tggagtgggt ggraactata tcatatgatg gaaggaatat acaatatgca 240

gactccgtga agggccgatg caccttctcc agagacaatt cttaggacac cctgtatctg 300

caactgaaca gcctcagacc ggaggacacg gctgtgtatt actgtgcgag acccgtaaga 360

agccgatggc tgcaattagg tcttgaagat gttttcata tctggggca ggggacaatg 420

gtcaccgtct cttcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480

aagagcacct ctggggcac acggggcctg ggctgcctgg tcaaggacta cttccccgaa 540

ccggtgacgg tgcgtggaa ctcaaggcgcc ctgaccagcg gctgcacac cttccccgt 600

gtcctacagt cctcaggact ctactccctc acgagcgtgg tgaccgtgcc ctccagcage 660

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720

aagaaaagtg agcccaaata ttgtgacaaa actcacacat gcccacccgtg cccagcacct 780

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 840

atctccccga cccctgaggt cacatcggtg gtggtgacg tgagccacga agaccctgag 900

gtcaagttca actggtagt ggacggcggt gaggtgcata atgccaagac aaagccgcgg 960

gaggagcagt acaacagcac gtaccgtgtg gtcaagcgtcc tcaccgtctt gaagcaggac 1020

tggctgaatg gcaaggagta caagtgcag gtctccaaca aagccctccc agccccatc 1080

gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgtt caccctgccc 1140

ccatccccggg atgagctgac caagaacctg gtcaagcctga cctgcctggt caaaggcttc 1200

tatccccatc acatcgccgt ggagtggtggag agcaatgggc agccggagaa caactacaag 1260

accacgcctc ccgtgctgga ctccgacggc tctttttcc tctacagcaa gtcaccgtg 1320

gacaagagca ggtggcagca ggggaacgtc ttctcatgtt ccgtgatgca tgaggctctg 1380

cacaacaatc acacccagaa cacccttcctt cttttttttt gtaaaatag 1428

<210> 2
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<223> Peptide sequence of double mutant His310-H435Lys.

<400> 2

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35 40 45

Lys Asn Tyr Ala Met His Trp Val Arg Gln Ala Pro Ala Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Arg Asn Ile Gln Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Cys Thr Phe Ser Arg Asp Asn Ser Gln Asp
85 90 95

Thr Leu Tyr Leu Gln Leu Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Pro Val Arg Ser Arg Trp Leu Gln Leu Gly Leu
115 120 125

Glu Asp Ala Phe His Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
260 265 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
275 280 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu Lys Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

405

410

415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Lys Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

4

1

WASH_6680526.1